<110> MA, Jing
        GUO, Yajun

<120> PREPARATION AND APPLICATION OF
        ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS

<130> 047630-0301

<140> US 10/723,003
<141> 2003-11-26

<150> CN 2003101199300
<151> 2003-11-25

<150> CN 031292909
<151> 2003-06-13

<160> 70

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 546
<212> DNA
<213> Homo sapiens

<400> 1
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agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca
540
gccccg
546

<210> 2
<211> 182
<212> PRT
<213> Homo sapiens

<400> 2

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Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1               5               10              15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20              25              30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35              40              45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50              55              60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65              70              75              80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
            85              90              95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100             105             110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115             120             125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130             135             140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145             150             155             160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
            165             170             175
Thr Ala Pro Thr Ala Pro
            180


<210> 3
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 3
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg
60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca
540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa
600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc
660
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2

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tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc
720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag
780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgcccccca
960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat
1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc
1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctcccggta aa
1242


<210> 4
<211> 414
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1               5                   10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                 185                 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        195                 200                 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
```

3

```
        210                     215                     220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                     230                     235                     240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                245                     250                     255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                260                     265                     270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                275                     280                     285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                290                     295                     300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                     310                     315                     320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                325                     330                     335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                340                     345                     350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
                355                     360                     365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                370                     375                     380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385                     390                     395                     400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                405                     410


<210> 5
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5
ggcggtggag gctctggtgg aggcggttca ggaggcggtg gatct
45

<210> 6
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1               5                   10                  15


<210> 7
<211> 426
<212> DNA
<213> Mus musculus
```

4

<400> 7
atcgccgcca ccatggaatg gagttggata tttctctttc tcctgtcagg aactgcaggt
60
gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca
120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg
180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc
240
actaagtaca tgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc
300
acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc
360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc
420
tcctca
426

<210> 8
<211> 138
<212> PRT
<213> Mus musculus

<400> 8
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1   5   10   15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20   25   30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35   40   45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
    50   55   60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65   70   75   80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
                85   90   95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
            100   105   110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
        115   120   125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser
    130   135

<210> 9
<211> 465
<212> DNA
<213> Mus musculus

<400> 9
atcatcacca gaacagctta cgagcagacc gccagacagc tcacagggat caagcttgcc
60
gccaccatgg aatcacagac tcaggtcttc ctctccctgc tgctctgggt atctggtacc
120
tgtgggaaca ttatgatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaag
180

5

gtcactatga gctgtaagtc cagtcaaagt gttttataca gttcaaatca gaagaactac
240
ttggcctggt accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc
300
actagggaat ctggtgtccc tgatcgcttc acaggcagtg atctgggac agattttact
360
cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc
420
tcctcataca cgttcggagg ggggaccaag ctggaaataa agcgg
465

<210> 10
<211> 133
<212> PRT
<213> Mus musculus

<400> 10
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1   5   10   15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
            20   25   30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
            35   40   45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    50   55   60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65   70   75   80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
            85   90   95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
            100   105   110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
            115   120   125
Leu Glu Ile Lys Arg
        130

<210> 11
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11
atcgccgcca ccatggaatg gagttggata tttctctttc tcctgtcagg aactgcaggt
60
gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca
120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg
180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc
240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc
300

acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc
360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc
420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccacccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg
1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980

actacacgca gaagagcctc tccctgtctc ccggtaaatg a

2021

<210> 12
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1   5   10   15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20   25   30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35   40   45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
    50   55   60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65   70   75   80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
                85   90   95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
            100   105   110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
            115   120   125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130   135   140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145   150   155   160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
                165   170   175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180   185   190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            195   200   205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210   215   220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225   230   235   240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245   250   255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260   265   270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            275   280   285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290   295   300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305   310   315   320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            325   330   335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340   345   350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

8

```
         355                    360                    365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                    375                    380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                    390                    395                    400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                   405                    410                    415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                   420                    425                    430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                   435                    440                    445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                   450                    455                    460
Ser Pro Gly Lys
465


<210> 13
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 13
atcatcacca gaacagctta cgagcagacc gccagacagc tcacagggat caagcttgcc
60
gccaccatgg aatcacagac tcaggtcttc ctctccctgc tgctctgggt atctggtacc
120
tgtgggaaca ttatgatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaag
180
gtcactatga gctgtaagtc cagtcaaagt gttttataca gttcaaatca gaagaactac
240
ttggcctggt accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc
300
actagggaat ctggtgtccc tgatcgcttc acaggcagtg gatctgggac agattttact
360
cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc
420
tcctcataca cgttcggagg ggggaccaag ctggaaataa agcggactgt ggctgcacca
480
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg
540
tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc
600
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac
660
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc
720
tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag
780
tgttag
786


<210> 14
<211> 239
```

9

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
 1   5   10   15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
            20   25   30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
        35   40   45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    50   55   60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65   70   75   80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
                85   90   95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
           100   105   110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
        115   120   125
Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130   135   140
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145   150   155   160
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165   170   175
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180   185   190
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195   200   205
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210   215   220
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225   230   235

<210> 15
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt
60
gtccactccc aggtgcagct ggtgcagtct ggcggtggag tggtccagcc cggccgcagc
120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg
180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgcctta taatgacggt
240

```
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca
300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgccgtata ctattgtgtg
360
cgcggcagcc gttacgactg gtacttggac tactgggggcc aaggcactcc agtcaccgtc
420
tcctct
426
```

```
<210> 16
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
 1               5                  10                  15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
            20                  25                  30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65                  70                  75                  80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
                85                  90                  95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
                100                 105                 110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
            115                 120                 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser
        130                 135
```

```
<210> 17
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 17
gagcattacc ggccatactc atcaccatcc caggatatct ctagaaagct tgccgccacc
60
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcc
120
agaggaaaca tcatgatgac tcagagccca tccagcttga gcgcatcagt aggcgaccgc
180
gtaacgatca cttgcaaatc ctctcagtca gtattgtact ccagcaacca gaagaactac
240
ctggccggat atcagcagac tcccggcaaa gccccaaagt tgctgattta ttgggcctcc
300
```

11

acgcgcgagt ctggcgtgcc atcacgcttt agcggcagcg ggtccggtac agattacacg
360
tttaccatta gcagtctgca gcctgaggac atagccacct actactgtca ccagtacttt
420
agttcctaca cttttggcca gggaactaaa ctgcagatta ctcga
465

<210> 18
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1   5   10   15
Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser
            20   25   30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser
        35   40   45
Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
    50   55   60
Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser
65   70   75   80
Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
                85   90   95
Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
            100   105   110
Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly
        115   120   125
Thr Lys Leu Gln Ile Thr Arg
    130   135

<210> 19
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt
60
gtccactccc aggtgcagct ggtgcagtct ggcggtggag tggtccagcc cggccgcagc
120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg
180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgcctta taatgacggt
240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca
300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgccgtata ctattgtgtg
360

cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc
420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctggggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag accctgccc ctgacctaag
1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg
1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc cggtaaatg a
2021

<210> 20
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20
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Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
  1               5                  10                  15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
                20                  25                  30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
            35                  40                  45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        50                  55                  60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65                  70                  75                  80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
                85                  90                  95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
        115                 120                 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130                 135                 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
                165                 170                 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180                 185                 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
        195                 200                 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210                 215                 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225                 230                 235                 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245                 250                 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
```

14

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385   390   395   400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405   410   415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                420   425   430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            435   440   445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        450   455   460
Ser Pro Gly Lys
465

<210> 21
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 21
gagcattacc ggccatactc atcaccatcc caggatatct ctagaaagct tgccgccacc
60
atggatttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcc
120
agaggaaaca tcatgatgac tcagagccca tccagcttga gcgcatcagt aggcgaccgc
180
gtaacgatca cttgcaaatc ctctcagtca gtattgtact ccagcaacca gaagaactac
240
ctggccggat atcagcagac tcccggcaaa gccccaaagt tgctgattta ttgggcctcc
300
acgcgcgagt ctggcgtgcc atcacgcttt agcggcagcg ggtccggtac agattacacg
360
tttaccatta gcagtctgca gcctgaggac atagccacct actactgtca ccagtacttt
420
agttcctaca cttttggcca gggaactaaa ctgcagatta ctcgaactgt ggctgcacca
480
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg
540
tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc
600
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac
660
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc
720
tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag
780
tgttag
786

<210> 22
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser
            20   25   30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser
        35   40   45
Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
    50   55   60
Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser
65   70   75   80
Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
                85   90   95
Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
            100   105   110
Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly
        115   120   125
Thr Lys Leu Gln Ile Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile
    130   135   140
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
145   150   155   160
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
                165   170   175
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
            180   185   190
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
        195   200   205
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
    210   215   220
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
225   230   235   240
Cys

<210> 23
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 23
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt
60
gtccactccc aggtgcagct ggtgcagtct ggcggtggag tggtccagcc cggccgcagc
120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg
180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgcctta taatgacggt
240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca
300

```
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgccgtata ctattgtgtg
360
cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc
420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctgggggca gcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg
1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
```

17

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actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac
2040
acagccccat ctcctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc
2100
aagattaccc agtcaccgtg cctccaacc tgcaggacga ggagctctgc gggggcctct
2160
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga
2220
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc
2280
agcccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga
2340
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc
2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggcccc
2460
tggaggccac agccccgaca gccccgtga
2489


<210> 24
<211> 624
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
1               5                   10                  15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
                20                  25                  30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
            35                  40                  45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
        50                  55                  60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65                  70                  75                  80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
                85                  90                  95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
            115                 120                 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        130                 135                 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
            165                 170                 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180                 185                 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            195                 200                 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        210                 215                 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
```

```
225                   230                   235                   240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245                   250                   255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                260                   265                   270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                275                   280                   285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290                   295                   300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                   310                   315                   320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                   330                   335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                340                   345                   350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                355                   360                   365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                   375                   380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                   390                   395                   400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                   410                   415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                420                   425                   430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                435                   440                   445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                   455                   460
Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
465                   470                   475                   480
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
                485                   490                   495
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys
                500                   505                   510
Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu
                515                   520                   525
Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn
    530                   535                   540
Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser
545                   550                   555                   560
Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr
                565                   570                   575
Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe
                580                   585                   590
Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro
                595                   600                   605
Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
    610                   615                   620
```

<210> 25
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>

19

<223> Synthetic Construct

<400> 25
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt
60
gtccactccc aggtgcagct ggtgcagtct ggcggtggag tggtccagcc cggccgcagc
120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg
180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgcctta taatgacggt
240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca
300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgccgtata ctattgtgtg
360
cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc
420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctgggggca gcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
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cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
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780
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840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
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1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620

20

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gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct cctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc cggtaaagg cggtggaggc tctggtggag
2040
gcggttcagg aggcggtgga tctacccagg actgctcctt ccaacacagc cccatctcct
2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat acccagtca
2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg
2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg
2280
agcgcgtgaa cacggagata cactttgtca ccaaatgtgc ctttcagccc cccccagct
2340
gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg
2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc
2460
agcccgactc ctcaaccctg ccacccccat ggagtccccg gcccctggag gccacagccc
2520
cgacagcccc gtga
2534


<210> 26
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
1               5                   10                  15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
            20                  25                  30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65                  70                  75                  80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
                85                  90                  95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
            100                 105                 110
```

21

```
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
        115                 120                 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130                 135                 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
            165                 170                 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180                 185                 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
        195                 200                 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210                 215                 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225                 230                 235                 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
            245                 250                 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
        340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460
Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
465                 470                 475                 480
Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser
            485                 490                 495
Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp
            500                 505                 510
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly
            515                 520                 525
Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys
    530                 535                 540
Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr
545                 550                 555                 560
Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys
```

22

```
                565                     570                      575
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser
            580                     585                 590
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser
        595                     600                 605
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro
    610                     615                 620
Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
625                     630                 635
```

<210> 27
<211> 1986
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 27
```
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg
60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca
540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa
600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac caaggacac cctcatgatc
660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc
720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag
780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca
960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat
1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc
1080
```

```
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctcccggta acaggtgca gctggtgcag
1260
tctggcggtg gagtggtcca gcccggccgc agcctgaggc tgtcctgcaa ggcatctggc
1320
tacaccttca ccagctacgt gatgacatgg gtgcgccaag ccccccggaaa gggcctcgaa
1380
tggattggct acattgtgcc ttataatgac ggtactaagt acaatgaaaa gttcaagggc
1440
agatttacaa tatcaagtga caagagcaag tcaaccgcat tcctccaaat ggacagcttg
1500
cgtccagagg acaccgccgt atactattgt gtgcgcggca gccgttacga ctggtacttg
1560
gactactggg gccaaggcac tccagtcacc gtctcctctg gcggtggagg ctctggtgga
1620
ggcggttcag gaggcggtgg atctaacatc atgatgactc agagcccatc cagcttgagc
1680
gcatcagtag gcgaccgcgt aacgatcact tgcaaatcct ctcagtcagt attgtactcc
1740
agcaaccaga gaactacct ggccggatat cagcagactc ccggcaaagc cccaaagttg
1800
ctgatttatt gggcctccac gcgcgagtct ggcgtgccat cacgctttag cggcagcggg
1860
tccggtacag attacacgtt taccattagc agtctgcagc ctgaggacat agccacctac
1920
tactgtcacc agtactttag ttcctacact tttggccagg gaactaaact gcagattact
1980
cgatga
1986


<210> 28
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                  10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70              '   75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
```

24

```
              115                    120                    125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                     135                    140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                     150                    155                    160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                    170                    175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                    185                    190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        195                    200                    205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210                     215                    220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                     230                    235                    240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                245                    250                    255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            260                    265                    270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        275                    280                    285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290                     295                    300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                     310                    315                    320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                325                    330                    335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340                    345                    350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        355                    360                    365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370                     375                    380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385                     390                    395                    400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gln Val
                405                    410                    415
Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu
            420                    425                    430
Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met
        435                    440                    445
His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr
    450                     455                    460
Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly
465                     470                    475                    480
Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln
                485                    490                    495
Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            500                    505                    510
Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Pro
        515                    520                    525
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    530                     535                    540
Gly Gly Gly Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ser
545                     550                    555                    560
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser
                565                    570                    575
```

```
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
            580                 585                 590
Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
            595                 600                 605
Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
            610                 615                 620
Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr
625                 630                 635                     640
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys
            645                 650                 655
Leu Gln Ile Thr Arg
            660
```

```
<210> 29
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 29
cttgccgcca ccatggaatg gagttggata tttctctttc tcctgtcagg aactgcaggt
60
gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca
120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg
180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc
240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc
300
acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc
360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc
420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctgggggca gcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
```

```
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg
1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac
2040
acagccccat ctcctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc
2100
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct
2160
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga
2220
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc
2280
agcccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga
2340
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc
2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggcccc
2460
tggaggccac agccccgaca gccccgtga
2489

<210> 30
<211> 624
<212> PRT
<213> Artificial Sequence

<220>
```

27

<223> Synthetic Construct

<400> 30
```
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1               5                   10                  15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
    50                  55                  60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65                  70                  75                  80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
            85                  90                  95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
        115                 120                 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130                 135                 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
            165                 170                 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180                 185                 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            195                 200                 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210                 215                 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225                 230                 235                 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
            245                 250                 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            275                 280                 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
```

28

```
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440             445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        450                 455             460
Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
465                 470             475                 480
Ser Asp Phe Ala Val Lys·Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
                485             490                 495
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys
            500             505             510
Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu
        515             520             525
Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn
        530             535             540
Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser
545             550             555                 560
Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr
            565             570             575
Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe
        580             585             590
Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro
        595             600             605
Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
    610             615             620


<210> 31
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 31
cttgccgcca ccatggaatg gagttggata tttctctttc tcctgtcagg aactgcaggt
60
gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca
120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg
180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc
240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc
300
acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc
360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc
420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctgggggca gcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
```

29

```
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg agggaggggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
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1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcagggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc cggtaaagg cggtggaggc tctggtggag
2040
gcggttcagg aggcggtgga tctacccagg actgctcctt ccaacacagc cccatctcct
2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat tacccagtca
2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg
2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg
2280
agcgcgtgaa cacggagata cactttgtca ccaaatgtgc ctttcagccc cccccccagct
2340
```

30

gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg
2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc
2460
agcccgactc ctcaaccctg ccaccccat ggagtccccg gcccctggag gccacagccc
2520
cgacagcccc gtga
2534

<210> 32
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1   5   10   15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
             20   25   30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
         35   40   45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
     50   55   60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65   70   75   80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
                 85   90   95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
             100   105   110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
         115   120   125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
     130   135   140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145   150   155   160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
             165   170   175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
             180   185   190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
         195   200   205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
         210   215   220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225   230   235   240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
             245   250   255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
             260   265   270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
         275   280   285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
         290   295   300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr

31

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325   330   335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340   345   350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355   360   365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370   375   380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385   390   395   400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405   410   415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420   425   430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435   440   445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450   455   460
Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
465   470   475   480
Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser
                485   490   495
Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp
            500   505   510
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly
    515   520   525
Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys
    530   535   540
Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr
545   550   555   560
Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys
                565   570   575
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser
            580   585   590
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser
    595   600   605
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro
    610   615   620
Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
625   630   635

<210> 33
<211> 1986
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 33
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg
60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120

ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca
540
gcccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa
600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc
660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc
720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag
780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgcccca
960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat
1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc
1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctcccggta aagaggtcca gctgcagcag
1260
tctggacctg agctggtaaa gcctggggct tcagtgaaga tgtcctgcaa ggcttctgga
1320
tacacattca ctagctatgt tatgcactgg gtgaagcaga agcctgggca gggccttgac
1380
tggattggat atattgttcc ttacaatgat ggcactaagt acaatgagaa gttcaaaggc
1440
aaggccacac tgacttcaga caaatcctcc agcacagcct acatggagct cagcagactg
1500
acctctgagg actctgcggt ctattattgt gtctacggta gtaggtacga ctggtattta
1560
gatgtctggg gcgcagggac cacggtcacc gtctcctcag gcggtggagg ctctggtgga
1620
ggcggttcag gaggcggtgg atctaacatt atgatgacac agtcgccatc atctctggct
1680
gtgtctgcag gagaaaaggt cactatgagc tgtaagtcca gtcaaagtgt tttatacagt
1740
tcaaatcaga agaactactt ggcctggtac cagcagaaac cagggcagtc tcctaaactg
1800

```
ctgatctact gggcatccac tagggaatct ggtgtccctg atcgcttcac aggcagtgga
1860
tctgggacag attttactct taccatcagc agtgtacaag ctgaagacct ggcagtttat
1920
tactgtcatc aatatttctc ctcatacacg ttcggagggg ggaccaagct ggaaataaag
1980
cggtga
1986
```

<210> 34
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34
```
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1               5                   10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
            35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
            85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
            115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
            165                 170                 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                 185                 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            195                 200                 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210                 215                 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                 230                 235                 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            245                 250                 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            260                 265                 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    275                 280                 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290                 295                 300
```

34

```
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305             310             315             320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            325             330             335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340             345             350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            355             360             365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
            370             375             380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385             390             395             400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Val

                405             410             415
Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val
            420             425             430
Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met
            435             440             445
His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Asp Trp Ile Gly Tyr
    450             455             460
Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly
465             470             475             480
Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu
            485             490             495
Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Tyr
            500             505             510
Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp Gly Ala Gly Thr Thr
            515             520             525
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    530             535             540
Gly Gly Gly Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
545             550             555             560
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
            565             570             575
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
            580             585             590
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
            595             600             605
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
610             615             620
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
625             630             635             640
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
            645             650             655
Leu Glu Ile Lys Arg
            660
```

<210> 35
<211> 426
<212> DNA
<213> Mus musculus

<400> 35
gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac
60

```
tcccaggtac aactacagca gcctggggct gagctggtga agcctggggc ctcagtgaag
120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag
180
acacctggtc ggggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc
240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc
300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg
360
acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc
420
tctgca
426


<210> 36
<211> 140
<212> PRT
<213> Mus musculus

<400> 36
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
1               5                   10                  15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
    50                  55                  60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
            115                 120                 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
    130                 135                 140


<210> 37
<211> 390
<212> DNA
<213> Mus musculus

<400> 37
accatggatt ttcaagtgca gattttcagc ttcctgctaa tcagtgcttc agtcataatg
60
tccagaggac aaattgttct ctcccagtct ccagcaatcc tgtctgcatc tccaggggag
120
aaggtcacaa tgacttgcag ggccagctca agtgtaagtt acatccactg gttccagcag
180
aagccaggat cctcccccaa accctggatt tatgccacat ccaacctggc ttctggagtc
240
cctgttcgct tcagtggcag tgggtctggg acctcttact ctctcacaat cagtagagtg
300
```

```
gaggctgaag atgctgccac ttattactgc cagcagtgga ctagtaaccc acccacgttc
360
ggtggtggga ccaagctgga gatcaaacga
390


<210> 38
<211> 129
<212> PRT
<213> Mus musculus

<400> 38
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1               5                   10                  15
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
            20                  25                  30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
        35                  40                  45
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
    50                  55                  60
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
65                  70                  75                  80
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
                85                  90                  95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
                100                 105                 110
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            115                 120                 125
Arg


<210> 39
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39
gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac
60
tcccaggtac aactacagca gcctggggct gagctggtga gcctggggc ctcagtgaag
120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag
180
acacctggtc ggggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc
240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc
300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg
360
acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc
420
tctgcagcta gcaccaaggg cccatcggtc ttcccccctgg caccctcctc caagagcacc
480
```

```
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccacccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg
1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc ccggtaaatg a
2021

<210> 40
<211> 470
<212> PRT
<213> Artificial Sequence
```

38

<220>
<223> Synthetic Construct

<400> 40

```
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
 1               5                  10                 15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                 30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
    50                  55                  60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
        115                 120                 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
    130                 135                 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly
    290                 295                 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
Ser Thr Tyr Arg Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            325                 330                 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
        340                 345                 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
```

```
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
Ser Leu Ser Pro Gly Lys
465                 470


<210> 41
<211> 711

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41
accatggatt ttcaagtgca gattttcagc ttcctgctaa tcagtgcttc agtcataatg
60
tccagaggac aaattgttct ctcccagtct ccagcaatcc tgtctgcatc tccaggggag
120
aaggtcacaa tgacttgcag ggccagctca agtgtaagtt acatccactg gttccagcag
180
aagccaggat cctcccccaa accctggatt tatgccacat ccaacctggc ttctggagtc
240
cctgttcgct tcagtggcag tgggtctggg acctcttact ctctcacaat cagtagagtg
300
gaggctgaag atgctgccac ttattactgc cagcagtgga ctagtaaccc acccacgttc
360

ggtggtggga ccaagctgga gatcaaacga actgtggctg caccatctgt cttcatcttc
420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac
480
ttctatccca gagaggccaa agtacagtgg aaggtggata cgccctcca atcgggtaac
540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc
600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat
660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g
711


<210> 42
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
```

```
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
            20                  25                  30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
            35                  40                  45
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
            50                  55                  60
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
65                  70                  75                  80
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
                85                  90                  95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
            100                 105                 110
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            115                 120                 125
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
            130                 135                 140
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            195                 200                 205
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser

    210                 215                 220
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210> 43
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 43
gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac    60
tcccaggtac aactacagca gcctggggct gagctggtga gcctggggc ctcagtgaag    120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag    180
acacctggtc ggggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc    240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc    300
tacatgcagc tcagcagćct gacatctgaa gactctgcgg tctattactg tgcaagatcg    360
acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc    420
tctgcagcta gcaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc    480
```

tctggggggca cagcggcccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
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780
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840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaagggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
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1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac
2040
acagccccat ctcctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc
2100
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct
2160

42

```
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga
2220
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc
2280
agccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga
2340
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc
2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggcccc
2460
tggaggccac agccccgaca gccccgtga
2489
```

<210> 44
<211> 626
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 44

```
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
1               5                   10                  15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
    50                  55                  60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
        115                 120                 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
    130                 135                 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
```

Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly
    290   295   300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305   310   315   320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            325   330   335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340   345   350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    355   360   365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370   375   380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385   390   395   400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            405   410   415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420   425   430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            435   440   445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450   455   460
Ser Leu Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro
465   470   475   480
Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu
            485   490   495
Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu
            500   505   510
Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu
    515   520   525
Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg
    530   535   540
Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro
545   550   555   560
Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln
            565   570   575
Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln
            580   585   590
Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr
            595   600   605
Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr
    610   615   620
Ala Pro
625

<210> 45
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 45

44

gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac
60
tcccaggtac aactacagca gcctggggct gagctggtga agcctggggc ctcagtgaag
120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag
180
acacctggtc ggggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc
240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc
300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg
360
acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc
420
tctgcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctggggca gcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
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780
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840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc
900
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960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccacccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
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1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccaçctcca
1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680

```
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc cggtaaagg cggtggaggc tctggtggag
2040
gcggttcagg aggcggtgga tctacccagg actgctcctt ccaacacagc cccatctcct
2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat tacccagtca
2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg
2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg
2280
agcgcgtgaa cacggagata cactttgtca ccaaatgtgc ctttcagccc cccccagct
2340
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2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc
2460
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2520
cgacagcccc gtga
2534

<210> 46
<211> 641
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 46
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
1               5                   10                  15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
    50                  55                  60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
        115                 120                 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
```

```
          130                      135                      140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                      150                      155                      160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                    165                      170                      175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
                    180                      185                      190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
                    195                      200                      205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
                    210                      215                      220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                      230                      235                      240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                    245                      250                      255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                    260                      265                      270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
                    275                      280                      285
Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly
                    290                      295                      300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                      310                      315                      320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                    325                      330                      335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                    340                      345                      350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
                    355                      360                      365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                    370                      375                      380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                      390                      395                      400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                    405                      410                      415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                    420                      425                      430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
                    435                      440                      445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                    450                      455                      460

Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465                      470                      475                      480
Gly Gly Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile
                    485                      490                      495
Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu
                    500                      505                      510
Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu
                    515                      520                      525
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg
                    530                      535                      540
Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val
545                      550                      555                      560
Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro
                    565                      570                      575
Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu
```

47

```
          580                   585                   590
Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn
          595                   600                   605
Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
          610                   615                   620
Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala
625                   630                   635                   640
Pro


<210> 47
<211> 1974
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 47
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg
60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca
540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa
600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc
660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc
720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag
780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgcccccca
960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat
1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc
1080
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```
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctcccggta aacaggtaca actacagcag
1260
cctggggctg agctggtgaa gcctggggcc tcagtgaaga tgtcctgcaa ggcttctggc
1320
tacacattta ccagttacaa tatgcactgg gtaaagcaga cacctggtcg gggcctggaa
1380
tggattggag ctatttatcc aggaaatggt gatacttcct acaatcagaa gttcaagggc
1440
aaggccacac tgactgcaga caaatcctcc agcacagcct acatgcagct cagcagcctg
1500
acatctgaag actctgcggt ctattactgt gcaagatcga cttactacgg cggtgactgg
1560
tacttcaatg tctggggcgc agggaccacg gtcaccgtct ctgcaggcgg tggaggctct
1620
ggtggaggcg gttcaggagg cggtggatct caaattgttc tctcccagtc tccagcaatc
1680
ctgtctgcat ctccagggga gaaggtcaca atgacttgca gggccagctc aagtgtaagt
1740
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1800
tccaacctgg cttctggagt ccctgttcgc ttcagtggca gtgggtctgg gacctcttac
1860
tctctcacaa tcagtagagt ggaggctgaa gatgctgcca cttattactg ccagcagtgg
1920
actagtaacc cacccacgtt cggtggtggg accaagctgg agatcaaacg atga
1974

<210> 48
<211> 657
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 48
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1               5                   10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
```

49

```
            130                      135                      140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                      150                      155                      160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                    165                      170                      175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
                180                      185                      190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            195                      200                      205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210                      215                      220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                      230                      235                      240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                    245                      250                      255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                260                      265                      270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            275                      280                      285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290                      295                      300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                      310                      315                      320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                    325                      330                      335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                340                      345                      350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            355                      360                      365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370                      375                      380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385                      390                      395                      400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gln Val
                    405                      410                      415
Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val
                420                      425                      430
Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met
            435                      440                      445
His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala
    450                      455                      460
Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly
465                      470                      475                      480
Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
                    485                      490                      495
Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
                500                      505                      510
Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
            515                      520                      525
Thr Thr Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
    530                      535                      540
Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
545                      550                      555                      560
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
                    565                      570                      575
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
                580                      585                      590
```

50

```
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
        595                 600                 605
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
        610                 615                 620
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
625                 630                 635                 640
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                645                 650                 655
Arg
```

```
<210> 49
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 49
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc
60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc
120
cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt
180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact
240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca
300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga
360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc
420
tcctcg
426
```

```
<210> 50
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 50
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1               5                   10                  15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20                  25                  30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
    50                  55                  60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65                  70                  75                  80
```

51

Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
                85   90   95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100   105   110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
        115   120   125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130   135   140

<210> 51
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc
60
agaggagaca tccagatgac ccagtccccg agctccctgt ccgcctctgt gggcgatagg
120
gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgtagcctg gtatcaacag
180
aaaccaggaa aagctccgaa actactgatt tactcggcat ccttcctcta ctctggagtc
240
ccttctcgct tctctggctc cagatctggg acggatttca ctctgaccat cagcagtctg
300
cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc
360
ggacagggta ccaaggtgga gatcaaacgt
390

<210> 52
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 52
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1   5   10   15
Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20   25   30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        35   40   45
Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
    50   55   60
Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
65   70   75   80
Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr
                85   90   95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln

```
              100                   105                   110
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
        115                   120                   125
Lys Arg
    130
```

<210> 53
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53
```
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc
60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc
120
cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt
180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact
240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca
300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga
360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc
420
tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctgggggca gcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg
1200
```

ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc cggtaaatg a
2021

<210> 54
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 54
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1   5   10   15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20   25   30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35   40   45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
    50   55   60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65   70   75   80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
                85   90   95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100   105   110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
            115   120   125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
    130   135   140

54

```
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145                 150                 155                 160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
                165                 170                 175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                180                 185                 190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
            195                 200                 205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
        210                 215                 220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225                 230                 235                 240
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
                245                 250                 255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
                260                 265                 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            275                 280                 285
Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
        290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                325                 330                 335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            340                 345                 350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        355                 360                 365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
370                 375                 380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                 390                 395                 400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405                 410                 415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            420                 425                 430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        435                 440                 445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        450                 455                 460
Ser Leu Ser Leu Ser Pro Gly Lys
465                 470


<210> 55
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 55
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc
60
agaggagaca tccagatgac ccagtccccg agctccctgt ccgcctctgt gggcgatagg
120
```

```
gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgtagcctg gtatcaacag
180
aaaccaggaa aagctccgaa actactgatt tactcggcat ccttcctcta ctctggagtc
240
ccttctcgct tctctggctc cagatctggg acggatttca ctctgaccat cagcagtctg
300
cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc
360
ggacagggta ccaaggtgga gatcaaacgt actgtggctg caccatctgt cttcatcttc
420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac
480
ttctatccca gagaggccaa agtacagtgg aaggtggata cgccctcca atcgggtaac
540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc
600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat
660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g
711


<210> 56
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct


<400> 56
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1               5                   10                  15
Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20                  25                  30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
            35                  40                  45
Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
        50                  55                  60
Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
65                  70                  75                  80
Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr
            85                  90                  95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            100                 105                 110
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            115                 120                 125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        130                 135                 140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            165                 170                 175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            195                 200                 205
```

56

```
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210> 57
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 57
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc
60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc
120
cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt
180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact
240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca
300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga
360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc
420
tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctgggggca gcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg aggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg
1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
```

```
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac
1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac
2040
acagccccat ctcctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc
2100
aagattaccc agtcaccgtg cctccaacc  tgcaggacga ggagctctgc ggggggcctct
2160
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga
2220
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc
2280
agcccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga
2340
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc
2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggcccc
2460
tggaggccac agccccgaca gccccgtga
2489

<210> 58
<211> 628
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 58
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20                  25                  30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
```

58

```
                35                        40                        45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
    50                        55                        60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65                        70                        75                        80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
                85                        90                        95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
                100                       105                       110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
                115                       120                       125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
                130                       135                       140
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145                       150                   ·     155                       160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
                165                       170                       175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                180                       185                       190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
                195                       200                       205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
                210                       215                       220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225                       230                       235                       240
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
                245                       250                       255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
                260                       265                       270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
                275                       280                       285
Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
                290                       295                       300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                       310                       315                       320
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                325                       330                       335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                340                       345                       350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
                355                       360                       365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                370                       375                       380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                       390                       395                       400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405                       410                       415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                420                       425                       430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
                435                       440                       445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                450                       455                       460
Ser Leu Ser Leu Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His
465                       470                       475                       480
Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp
```

59

```
                    485                    490                    495
Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp
            500                    505                    510
Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp
            515                    520                    525
Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu
        530                    535                    540
Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln
545                    550                    555                    560
Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
            565                    570                    575
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
            580                    585                    590
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
            595                    600                    605
Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala
        610                    615                    620
Pro Thr Ala Pro
625


<210> 59
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 59
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc
60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc
120
cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt
180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact
240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca
300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga
360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc
420
tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc
480
tctgggggca gcggccct gggctgcctg gtcaaggact acttccccga accggtgacg
540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc
660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt
720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc
780
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tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc
840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc
900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc
960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag
1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat
1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg
1140
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1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca
1260
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1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga
1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg
1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca
1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag
1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc
1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta
1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc
1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca
1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc
1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga
1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc
1980
actacacgca gaagagcctc tccctgtctc ccggtaaagg cggtggaggc tctggtggag
2040
gcggttcagg aggcggtgga tctacccagg actgctcctt ccaacacagc cccatctcct
2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat tacccagtca
2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg
2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg
2280
agcgcgtgaa cacggagata cactttgtca ccaaatgtgc ctttcagccc cccccagct
2340
gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg
2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc
2460

agcccgactc ctcaaccctg ccaccccat ggagtccccg gccctggag gccacagccc
2520
cgacagcccc gtga
2534

<210> 60
<211> 643
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 60
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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20                  25                  30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
    50                  55                  60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65                  70                  75                  80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
                85                  90                  95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
               100                 105                 110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
           115                 120                 125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
       130                 135                 140
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145                 150                 155                 160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
               165                 170                 175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
           180                 185                 190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
       195                 200                 205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
   210                 215                 220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225                 230                 235                 240
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
               245                 250                 255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
           260                 265                 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
       275                 280                 285
Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
   290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
               325                 330                 335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
```

62

```
                  340                    345                      350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
          355                    360                  365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
      370                    375                  380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                        390                  395                  400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
              405                    410                  415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
          420                    425                  430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
          435                    440                  445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
      450                    455                  460
Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
465                        470                  475                  480
Gly Ser Gly Gly Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser
              485                    490                  495
Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr
          500                    505                  510
Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu
          515                    520                  525
Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met
      530                    535                  540
Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu
545                        550                  555                  560
Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro
              565                    570                  575
Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu
          580                    585                  590
Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg
          595                    600                  605
Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser
      610                    615                  620
Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro
625                        630                  635                  640
Thr Ala Pro
```

<210> 61
<211> 1998
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 61
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg
60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180

63

gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca
540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa
600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc
660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc
720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag
780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgcccca
960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat
1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc
1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctcccggta aagaggttca gctggtggag
1260
tctggcggtg gcctggtgca gccagggggc tcactccgtt tgtcctgtgc agcttctggc
1320
ttcaacatta aagacaccta tatacactgg gtgcgtcagg ccccgggtaa gggcctggaa
1380
tgggttgcaa ggatttatcc tacgaatggt tatactagat atgccgatag cgtcaagggc
1440
cgtttcacta taagcgcaga cacatccaaa aacacagcct acctgcagat gaacagcctg
1500
cgtgctgagg acactgccgt ctattattgt tctagatggg aggggacgg cttctatgct
1560
atggactact ggggtcaagg aaccctggtc accgtctcct cggctagcac caagggccca
1620
tcggtcggcg gtggaggctc tggtggaggc ggttcaggag gcggtggatc tgacatccag
1680
atgacccagt ccccgagctc cctgtccgcc tctgtgggcg ataggttac catcacctgc
1740
cgtgccagtc aggatgtgaa tactgctgta gcctggtatc aacagaaacc aggaaaagct
1800
ccgaaactac tgatttactc ggcatccttc ctctactctg gagtccttc tcgcttctct
1860

```
ggctccagat ctgggacgga tttcactctg accatcagca gtctgcagcc ggaagacttc
1920
gcaacttatt actgtcagca acattatact actcctccca cgttcggaca gggtaccaag
1980
gtggagatca aacgttga
1998
```

<210> 62
<211> 665
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 62

```
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1               5                   10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
        130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro

145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                 185                 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            195                 200                 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        210                 215                 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                 230                 235                 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                245                 250                 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            260                 265                 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        275                 280                 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        290                 295                 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                 310                 315                 320
```

```
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                325             330             335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340             345             350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        355             360             365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370             375             380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385             390             395             400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Val
            405             410             415
Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
            420             425             430
Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile
        435             440             445
His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
    450             455             460
Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly
465             470             475             480
Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln
            485             490             495
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg
            500             505             510
Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            515             520             525
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Gly Gly
            530             535             540
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
545             550             555             560
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            565             570             575
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp
        580             585             590
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala
    595             600             605
Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser
    610             615             620
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
625             630             635             640
Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly
            645             650             655
Gln Gly Thr Lys Val Glu Ile Lys Arg
            660             665
```

<210> 63
<211> 1098
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 63
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg
60

66

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agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca
540
gccccgggcg gtggaggctc tggtggaggc ggttcaggag cggtggatc tgtgagagaa
600
agaggtcctc agagagtagc agctcacata actgggacca gaggaagaag caacacattg
660
tcttctccaa actccaagaa tgaaaaggct ctgggccgca aaataaactc ctgggaatca
720
tcaaggagtg ggcattcatt cctgagcaac ttgcacttga ggaatggtga actggtcatc
780
catgaaaaag ggttttacta catctattcc caaacatact ttcgatttca ggaggaaata
840
aaagaaaaca caaagaacga caaacaaatg gtccaatata tttacaaata cacaagttat
900
cctgacccta tattgttgat gaaaagtgct agaaatagtt gttggtctaa agatgcagaa
960
tatggactct attccatcta tcaaggggga atatttgagc ttaaggaaaa tgacagaatt
1020
tttgtttctg taacaaatga gcacttgata gacatggacc atgaagccag tttttttggg
1080
gcctttttag ttggctaa
1098


<210> 64
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 64
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                  10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
```

Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100   105   110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
            115   120   125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
        130   135   140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145   150   155   160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165   170   175
Thr Ala Pro Thr Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            180   185   190
Gly Gly Gly Gly Ser Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala
            195   200   205
His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
        210   215   220
Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
225   230   235   240
Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
                245   250   255
Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
            260   265   270
Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
        275   280   285
Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
        290   295   300
Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
305   310   315   320
Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
                325   330   335
Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
        340   345   350
Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
        355   360   365

<210> 65
<211> 1203
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg
60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac
120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc ggggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300

gtgaacacgg agatacactt tgtcaccaaa tgtgccttc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca
540
gccccgatga agcagatcga ggacaaaatt gaggaaatcc tgtccaagat ttaccacatc
600
gagaacgaga tcgcccggat taagaaactc attggcgaga cctctgagga aaccatttct
660
acagttcaag aaaagcaaca aaatatttct ccctagtga gagaaagagg tcctcagaga
720
gtagcagctc acataactgg gaccagagga agaagcaaca cattgtcttc tccaaactcc
780
aagaatgaaa aggctctggg ccgcaaaata aactcctggg aatcatcaag gagtgggcat
840
tcattcctga gcaacttgca cttgaggaat ggtgaactgg tcatccatga aaaagggttt
900
tactacatct attcccaaac atactttcga tttcaggagg aaataaaaga aaacacaaag
960
aacgacaaac aaatggtcca atatatttac aaatacacaa gttatcctga ccctatattg
1020
ttgatgaaaa gtgctagaaa tagttgttgg tctaaagatg cagaatatgg actctattcc
1080
atctatcaag ggggaatatt tgagcttaag gaaaatgaca gaatttttgt ttctgtaaca
1140
aatgagcact gatagacat ggaccatgaa gccagttttt ttggggcctt tttagttggc
1200
taa
1203

<210> 66
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 66
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1   5   10   15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20   25   30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35   40   45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50   55   60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65   70   75   80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
            85   90   95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100   105   110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser

69

```
          115                      120                      125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                  135                  140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                  150                  155                  160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                  170                  175
Thr Ala Pro Thr Ala Pro Met Lys Gln Ile Glu Asp Lys Ile Glu Glu
            180                  185                  190
Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys
            195                  200                  205
Lys Leu Ile Gly Glu Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
    210                  215                  220
Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg
225                  230                  235                  240
Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
                245                  250                  255
Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
            260                  265                  270
Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
            275                  280                  285
Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
    290                  295                  300
Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
305                  310                  315                  320
Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
                325                  330                  335
Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
            340                  345                  350
Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
            355                  360                  365
Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
    370                  375                  380
Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
385                  390                  395                  400
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<210> 67
<211> 1749
<212> DNA
<213> Artificial Sequence


<220>
<223> Synthetic Construct

<400> 67
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120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg
180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag
240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc
300
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gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt
360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg
420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc
480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca
540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa
600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac caaggacac cctcatgatc
660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc
720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag
780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg
840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag
900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgcccca
960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat
1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc
1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac
1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac
1200
aaccactaca cgcagaagag cctctccctg tctcccggta aagtgagaga aagaggtcct
1260
cagagagtag cagctcacat aactgggacc agaggaagaa gcaacacatt gtcttctcca
1320
aactccaaga atgaaaaggc tctgggccgc aaaataaact cctgggaatc atcaaggagt
1380
gggcattcat tcctgagcaa cttgcacttg aggaatggtg aactggtcat ccatgaaaaa
1440
gggtttttact acatctattc ccaaacatac tttcgatttc aggaggaaat aaaagaaaac
1500
acaaagaacg acaaacaaat ggtccaatat atttacaaat acacaagtta tcctgaccct
1560
atattgttga tgaaaagtgc tagaaatagt tgttggtcta aagatgcaga atatggactc
1620
tattccatct atcaaggggg aatatttgag cttaaggaaa atgacagaat ttttgtttct
1680
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1740
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1749

<210> 68
<211> 582
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 68

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Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
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Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20              25              30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35              40              45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50              55              60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65              70              75              80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
            85              90              95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
        100             105             110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
    115             120             125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130             135             140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145             150             155             160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
            165             170             175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180             185             190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
    195             200             205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210             215             220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225             230             235             240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            245             250             255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    260             265             270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    275             280             285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290             295             300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305             310             315             320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            325             330             335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340             345             350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    355             360             365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370             375             380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385             390             395             400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Val Arg
            405             410             415
Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
            420             425             430
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Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
        435                 440                 445
Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
    450                 455                 460
Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
465                 470                 475                 480
Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
                485                 490                 495
Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
            500     .           505                 510
Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
        515                 520                 525
Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
        530                 535                 540
Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
545                 550                 555                 560
Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
                565                 570                 575
Gly Ala Phe Leu Val Gly
                580
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<210> 69
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 69
gcactcgagt tttacccgga gacagggaga g
31

<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 70
gagcccaaat cttgtgacaa aac
23